



FIG. I

IG-LIKE

M	NR1	MSSSCSGLTRVLVAVATALVSSS
M	IL-6R	MLTVGCTLLVALLAAPAVALLVLS
H	CNTR	MAAPVPWACCAVLAAA
H	IL-12p40	MCHQQLVISWESLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDG
M	GM-CSFR	MTSSHAMNITPLAQLALLFSTLLIPGTO

M	NR1	-VDWFERDGSRLLOQ
M	IL-6R	VTIHWVYSGSONR
H	CNTR	--VTWRVNGTDLA
H	IL-12p40	--ITWTLDOSSSEV
M	GM-CSFR	--LTWACDTAAGNVTVTCTVTSREAGIHRRVSPFGCRWFRRMMALHHGVTLDDVNGT

M	NR1	LKLGF
M	IL-6R	VDV
H	CNTR	LHVGL
H	IL-12p40	LHKKEDGIWSTDILKDQKE
M	GM-CSFR	VGGAAAHWRLLS-FVNESAA

A-----A

FIG. 2A

NUCLEIC ACID ENCODING α CHAIN OF HUMAN IL-11 RECEPTOR

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REPLACEMENT SHEET

A_____A

M	NR1	PPARPEVSCQAVDX-EMFSC	TWSPGQVSG	LPTRYLT	SYRKKTL	PGAESQ	RESPST	GPGWP
M	IL-6R	PPEPKLSCFRKNPLVMAI	CEWRPST	PSPTTKAVL	FAKKINT	TNGK	----	SDFQVP
H	CNTR	PPREPVLSCRSNTXPKGFYCS	WHLP	TPTYI	PNTFNV	TVLH	----	GSKIMV
H	IL-12p40	PKNKTFLRCEAKNYSGRFT	CWWLTTI	----	STDLT	FVKSSRGSS	----	DPQGVT
M	GM-CSFR	GSGAENLTCEIRAA-RFLSCA	WREGPAA	--PADVRY	SLRVLNST	----	----	GHDVAR

SD100A

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M NR1      CPQDPLE-----ASRCVHG-----AELWSEYRTNVTEVNPL--GASTCLLD
M IL-6R    CQYSQQLK-----SFSCQVE-----ILEGDKVYHIVSLCVANSVGSKSSHNE
H CNTFR    CEKDPAL-----KNRCHIRYMHLFSTIKYKVSFSVSNAL----GHNATAIT
H IL-12p40 CGAATLSAERVRGDNKEYEYSVEQCEDSACPAAKESLPIEVMVDV--HKLKYENYTSS
M GM-CSFR  CMADPGDDV-----ITQCIA-----NDLSLLGSEAYLVVTGRSGAGPVRFLDD

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M NR1          VRLQSTLR---
M IL-6R        AFHSLKMQV--
H CNTFR        FDEFTIVK---
H IL-12p40     FFIRDIK---
M GM-CSFR      VVATKALERLG

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FIG. 2B

A vertical line with the letter 'B' at both the top and bottom ends.

FIG. 2B

B

M NR1 PDPPQGLRVESVPGYPRRLHGSWTYPASWPRQPHFL-----LKLRLQXRPAQHPAWSTV
M IL-6R PDPPANLVVSAIPGRPRWLKVSQHPETWDPY-YL-----LQFQLRXPVWSKEFTVL
H CNTFR PDPPENVVARPVPSNPRRLEVITWQTPSTWDPDESFLKFF-LRYRPLILDQWQHVELSD
H IL-12p40 PDPPNNLQLK-PLKNSRQVEVSWEXPDWTWSTPHSYFSLTFCVQVQGKSREKKDRVFTD
M GM-CSFR --PPRDVT---ASCNSSHCTVSWAPPSTWASLTARDFQFE-VQWQSAEPGSTPRKVLVV

SD100B

M NR1 RPIGL--EEVITDAVAGLPMVRVSARDFLDAGTWSAWSPEAWGTPSTG-PLQDEIPD-
M IL-6R LLPVAQYQCVIHDAALRGVKMVVQVRGKEELDGLQWSEWSPEVTGTPWIAEPRTTPAGIL
H CNTFR GT-----AHTITDAYAGKEYIIQVAAKDNEI-GTWSWVAHAHATPWTEPRHLTTEAQ
H IL-12p40 KT-----SATVICRKNASISVRAQDRYYSSSWSEWASVPCS*
M GM-CSFR KETRL----AFPSAPHGGMKVVRAGDTRMK-HWGEWSPAHL-EAEDTRVP-----

M NR1 WSQGHGQQLVVVAQEDSPAPARPSLQDPRLDHRDPLEQ
M IL-6R WNPTQVSVEDSANHEDQYESSTEATSVLAPVQESSSSMSLPT
H CNTFR AAETTTSTTSSSLAPPPTTKIC-----
M GM-CSF -----

M NR1 VAVLASLLGIFSCGLGAVGALALGLWLRLRRSGKDGPKGLLA--PMIPVEKLPGIPN
M IL-6R FLVAGGSLAFGLLLCVFIIL-----RLKQWKSEAEKESKTTSPPPPYSGLGPKPT
H CNTFR DPGELSGGGPSAPFLVSVPI TLALAAAAATASSLLI*
M GM-CSF ALLYAVTACAVLLCALALGVTC-----RRFEVTR-----LYPPPIGIRD

TM/CYT

M NR1 LQRTPENFS*
M IL-6R FLLVPLLTPHSSGSDNTVNHSCLGVRDAQSPYDNSNRDYLFPF*
M GM-CSFR KVSDDVRVNPETLRKDILLQP*

C

FIG. 2C

TCTAACAGCC	TTACCCCACT	TGGTGCATCA	ATTTTCTCC	TAGGAAGCCT	CAGTTTGGG	60
GAGGAAGAGC	CAGGCTTTAG	CTCCCATCTC	AGGGGTCGGG	GATTTTGGAC	TCTACCTCTC	120
CCCACAG	ATG AGC AGC	TGC TCA GGG	CTG AGC AGG	GTC CTG GTG	GCC	169
Met	Ser Ser Ser	Cys Ser Gly	Leu Ser Arg	Val Leu Val	Ala	
1	5	5	10			
GTG GCT	ACA GCC	CTG GTG	TCT GCC	TCC CCC	TGC CCC	CAG GCC
Val	Ala Thr	Ala Leu	Val Ser	Ala Ser	Pro Ser	Cys Pro
15	20	20	25	30	30	30
GGC CCC	CCA GGC	GTC CAG	TAT GGG	CAG CCA	GGC AGG	TCC GTG
Gly	Pro pro	Gly Val	Gln Gln	Tyr Gly	Arg Ser	Val Lys
35	40	45	45	45	45	45
TGT TGT	CCT GGA	GTG ACT	GCC GGG	GAC CCA	GTG TCC	TGG TTT
Cys	Cys Pro	Gly Val	Thr Ala	Gly Asp	Pro Val	Ser Trp
50	55	55	60	60	60	60
GGG GAG	CCA AAG	CTG CTC	CAG GGA	CCT GAC	TCT GGG	CTA GGG
Gly	Glu Pro	Lys Leu	Leu Gln	Gly Pro	Asp Ser	Gly Leu
65	70	70	75	75	75	75
CTG GTC	CTG GCC	CAG GCA	GAC AGC	ACT GAT	GAG GGC	ACC TAC
Leu	Val Leu	Ala Ala	Gln Asp	Ser Thr	Thr Asp	Gly Thr
80	85	85	90	90	90	90
CAG ACC	CTG GAT	GGT GCA	CTT GGG	GGC ACA	GTG ACC	CTG CAG
Gln	Thr Leu	Leu Asp	Gly Ala	Leu Gly	Thr Val	Leu Thr
95	100	100	105	110	110	110

FIG. 8A

A

A

A

TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu 115 120 125	505
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC Asn Phe Ser Cys Thr Thr Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr 130 135 140	553
CGC TAC CTC ACC TCC TAC AGG AAG ACA GTC CTA GGA GCT GAT AGC Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser 145 150 155	601
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC Gln Arg Arg Ser Pro Ser Thr Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro 160 165 170	649
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln 175 180 185 190	697
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA Tyr Arg Ile Asn Val Thr Glu Val Val Asn Pro Leu Gly Gly Ala Ser Thr 195 200 205	745
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro 210 215 220	793
CAG GGC CTG CCG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg 225 230 235	841

B

FIG.8B

B

GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu 240 245 250	889
CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG TCC Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser 255 260 265 270	937
ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala 275 280 285	985
GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala 290 295 300	1033
GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr 305 310 315	1081
GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln 320 325 330	1129
CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser 335 340 345 350	1177
CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln 355 360 365	1225

C

FIG.8C

09/532,263

**NUCLEIC ACID ENCODING α CHAIN OF
HUMAN IL-11 RECEPTOR**

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REPLACEMENT SHEET

1273	GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG GTG Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val 370 375 380
1321	GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly 385 390 395
1369	AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val 400 405 410
1416	GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT Asp Arg Arg Pro Gly Ala Pro Asn Leu 415 420
1476	CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA
1536	GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGGG GCCCATTTCT GTGAGACCCT
1596	GTATTTTCAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTCACCCCA GAGTTGGAGT
1656	TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG
1716	AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG
1776	TCCTTGGCTC TTGGCCCTTC CCCTTGCAGG GGTGTGTCAG GTGTGAATAA AGAGAATAAG
1800	GAAGTTCTTG GAGATTATAC TCAG

FIG. 8D